

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACACCACCGGACAT  
 CTCGGGAGCTGCTGGGTGCAAAGAAGACCCACACCTCACAATTGAAGTGATCCCTTGCAAGATCTGTGG  
 GGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGTGAGGGGTGCAAGGGCTTCTTCCGCCGCAGC  
 CAGCAGTGTAATGTGGCCTACTCCTGCACGCGTCAGCAGAACTGCCCCATTGACCGAACCAGCCGCAACC  
 GATGCCAGCATTGCCGCCTGCAGAAGTGCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCG  
 AATGTCCAAGAAGCAGAGGGACAGTCTACATGCAGAAGTGCAAAACAAGTGAACAGCAGCAGCAACAG  
 GAACAAGTGGCCAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTACATACACTTTAGGGCTCT  
 CAGATGGGCAGCTACCACTGGGCGCCTCACCTGACCTACCCGAGGCCTCTGCTTGTCCCCCTGGCCTCCT  
 GAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTGGCCAAAACAGAGGTCCAGGGGGCCTCCTGC  
 CACCTTGAGTAGTAGTCCAGAACGAGGCAAAGCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAAC  
 TTACTCTTGGAAGATGTGGACTTCGTTTTTGAGGAAACCAGGCATCCTGAACTTGGGGAACCAGAACAGGG  
 TCCAGACAGCCACTGCATTCCCAGTTTCTGCAGTGCCCCAGAGGTACCATATGCCTCTCTGACAGACATA  
 GAGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGCATGCCAGCTGCGACTGGAGGACCTTCTAC  
 GGCAGCGCACCAACCTCTTTTTCACGGGAGGAGGTGACAGCTACCAGAGGAAGTCAATGTGGGAGATGTG  
 GGAGCGCTGTGCCCACCACCTCACTGAGGCCATTGAGTATGTGGTGGAGTTTGCCAAGCGGCTTTGAGGC  
 TTCATGGAGCTCTGCCAGAATGACCAGATCATACTACTGACAGCAGGAGCAATGGAAGTCGTCTAGTCA  
 GAATGTGCAGGGCCTACAATGCCAACAACCACACAGTCTTTTTTTGAAGGCAAATACGGTGGTGTGGAGCT  
 GTTTTCGAGCCTTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCACTTCTCAGCGCCCTG  
 TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGTCTCTGGGCTCC  
 AAGAGAAGAGGAGAGTGGAAACATCTGCAATACAATTTGGAAGTGGCTTTCCATCATCATCTCTGCAAGAC  
 TCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGAAAACCTCCGGAGCCTGTGCAGCCAACATGTG  
 GAAAAGCTGCAGATCTTCCAGCACCTCCACCCCATCGTGGTCCAAGCCGCCTTCCCNCCACTCTATAAGG  
 AACTCTTCAGCACTGATGTTGAATCCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACCTTTCTA  
 TTTCTTCAGCCCTCTGACCCGTCTCCCTGGACTCCCTTCACCCAGCCTTTCCCTTTCTGCACTCTATGA  
 AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCCTAGGCTTGCCTTGTAGGACA  
 ACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTTCCCATAGTTCACCCCTGGCTTCTGGAA  
 GCTGTGGGGTAGATGGGATAGAGATAGGATGACCAAGTCAAATAAAAAACAGACTGACAATCAGCAGGGA  
 TAAATCCAGGTACCTGGGATAAGGAGAACTCAAATCTAGGCTTGAAAGCTAATAACAGTCCCTTTCAATAC  
 CTCATTGTATTTCCCATGGGTCTCTCTGGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCC  
 AGAAGGACCTGTATATAATAAGAATATAGATTCCCTG (SEQ ID NO:1)

MDRAPQRHHRTSRELLAAKKTHTSQIEVIPCKICGDKSSGIHYGVITCEGCKGFFRRSQQCNVAYS  
 CTRQQNCPIDRTSRNRCQHCRLOKCLALGMSRDAVKFGRMSKKQRDSLHAEVQKQLQQQQQQE  
 QVAKTPPAGSRGADTLTYTLGLSDGQLPLGASPDLPASACPPGLLRASGSGPPYSNTLAKTEVQG  
 ASCHLEYSPERGKAEGRDSIYSTDGQLTLGRCGLRFEETRHPHELGEPEQGPDSHCIPSFCSPAEPY  
 ASLTDIEYLVQNVCKSFRETCLRLDLLRQRTNLFREEVTSYQRKSMWEMWERCAHHLTEAIQ  
 YVVEFAKRLSGFMELCQNDQILLTAGAMEVVLVRMCRAYNANNHTVFFEGKYGGVELFRALGC  
 SELISSIFDFSHFLSALCFSEDEIALYALVLINANRPGLEKRRVEHLQYNLELAFHHHLCKTHRQG  
 LLAKLPKGLRLSLCSQHVEKLQIFQHLHPVVQAAPPLYKELFSTDVESPEGLSK (SEQ ID NO:2)

FIG. 1

underlined = deleted in targeting construct

green = sequence flanking Neo insert in targeting construct

GGAGGGCAGCAAGGACGGCACCAAGGGAGCTACCCCATGGACAGGGCCCCACAGAGACAC  
CACCGGACATCTCGGGAGCTGCTGGCTGCAAAGAAGACCCACACCTCACAAATTGAAGTG  
ATCCCTTGCAAGATCTGTGGGGACAAGTCATCTGGGATCCACTACGGGGTTATCACCTGT  
GAGGGGTGCAAG [GGCTTCTTCCGCCGAGCCAGCAGTGTAAATGTGGCCTACTCCTGCACG  
CGTCAGCAGAA] CTGCCCCATTGACCGAACCAGCCGCAACCGATGCCAGCATTGCCGCCTG  
CAGAAGTGCCTGGCTCTGGGCATGTCCCGAGATGCTGTCAAGTTTGGCCGAATGTCCAAG  
AAGCAGAGGGACAGTCTACATGCAGAAGTGCAGAAACAACCTGCAACAGCAGCAGCAACAG  
GAACAAGTGGCCAAAGACTCCTCCAGCTGGGAGCCGCGGAGCAGACACACTTA [CATACACT  
TTAGGGCTCTCAGATGGGCAGCTACCACTGGGGCGCCTCACCTGACCTACCCGAGGCCTCT  
GCTTGTCCCCCTGGCCTCCTGAGAGCCTCAGGCTCTGGCCCACCATATTCCAATACCTTG  
GCCAAAACAGAGGTCCAGGGGGCCTCCTGCCACCTTGAGTATAGTCCAGAACGAGGCAAA  
GCTGAAGGCAGAGACAGCATCTATAGCACTGACGGCCAACCTTACTCTTGGAAGATGTGGA  
CTTCGTTTTGAGGAAACCAGGCATCCTGAACCTTGGGGAACCAGAACAGGGTCCAGACAGC  
CACTGCATTCCCAAGTTTCTGCAGTGGCCAGAGGTACCATATGCCTCTCTGACAGACATA  
G] AGTACCTGGTACAGAATGTCTGCAAGTCCTTCCGAGAGACATGCCAGCTGCGACTGGAG  
GACCTTCTACGGCAGCGCACCAACCTCTTTTTCACGGGAGGAGGTGACCAGCTACCAGAGG  
AAGTCAATGTGGGAGATGTGGGAGCGCTGTGCCACCACCTCACTGAGGCCATTCACTAT  
GTGGTGGAGTTTGCCAAAGCGGCTTTTCAAGGCTTCATGGAGCTCTGCCAGAATGACCAGATC  
ATACTACTGACAGCAGGAGCAATGGAAGTCGTCCTAGTCAGAATGTGCAGGGCCTACAAT  
GCCAACAAACCACACAGTCTTTTTTGAAGGCAATACGGTGGTGTGGAGCTGTTTCGAGCC  
TTGGGCTGCAGCGAGCTCATCAGCTCCATATTTGACTTTTCCCCTTCTCAGCGCCCTG  
TGTTTTTCTGAGGATGAGATTGCCCTCTACACGGCCCTGGTTCTCATCAATGCCAACCGT  
CCTGGGCTCCAAGAGAAGAGGAGAGTGAACATCTGCAATACAATTTGGAAGTGGCTTTC  
CATCATCATCTCTGCAAGACTCATCGACAAGGCCTCCTAGCCAAGCTGCCACCCAAAGGA  
AACTCCCGAGCCTGTGCAGCCAACATGTGGAAGAGCTGCAGATCTTCCAGCACCTCCAC  
CCCATCGTGGTCCAAGCCGCTTCCNCCACTCTATAAGGAACTCTTCAGCACTGATGTT  
GAATCCCCCTGAGGGGCTGTCAAAGTGATCTGGAGGAAGGACAACCTTCTATTTCTTCAG  
CCCTCTGACCCGCTCTCCCTGGACTCCCTTCAACCCAGCCTTTCCCTTTCTGCACTCTATGA  
AGGGTGGTATCCCTAGGAGTAAGCAAATCCTAAGACTGATTTTCTGCCCCCTAGGCTTGCC  
TTGTAGGACAACAGCAGCAAGTGATGGAGAAAAGGCTTGTTATGTTTGATTTCCCATAG  
TTCCACCCTGGCTTCTGGAAGCTGTGGGGTAGATGGGATAGAGATAGGATGACCAAGTCA  
AATAAAAAACAGACTGACAATCAGCAGGGATAAATCCAGGTACCTGGGATAAGGAGAACT  
CAAATCTAGGCTTGAAAGCTAATAACAGTCCCTTTCAATACCTCATTGTATTTCCCCATGG  
GTCTCTCTGGGGGGACATGGATCTAGCTCAGAGACTGGTGGCAAGCCCCCAGAAGGACCT  
GTATATAATAAGAATATAGATTCCCTG (SEQ ID NO:1)

FIG. 2A

Gene Sequence  
Structure \*

252 bp

Sequence Deleted

472 bp

Size of full-length  
cDNA: 2066 bp



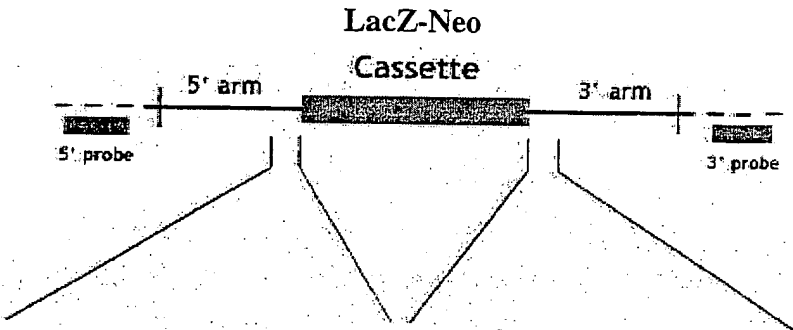
Targeting Vector\* (genomic sequence)

Construct Number: 651

Arm Length:

5': 1.6 kb

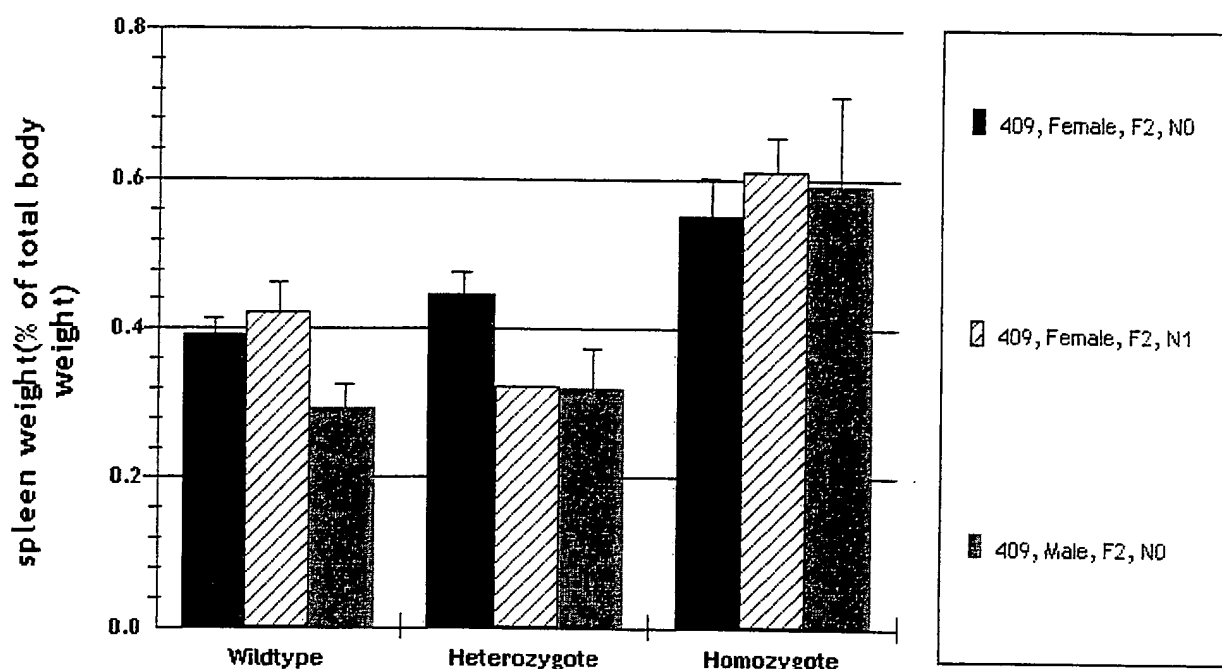
3': 2.5 kb



5'>CAGGGTCCATCACAATTATAC AGTGGAGGTTCGGGGACTTTGGTG GATGTAGAAATTCCTTGAGACCAGT GCACATGAATTGGAGGTCCCTGGG ACCACCTCAAACCTCCGAGAGGGTG GGATAAGCAGTTTCTGTTTCCAG GGCTTCTTCGCGCCGAGCCAGCAG TGTAATGTGGCCTACTCCTGCACG CGTCAGCAGAA<3' (SEQ ID NO: 3)	5'>CATACACTTTAGGGCTCTCAG ATGGGCAGCTACCACTGGGCGCCT CACCTGACCTACCCGAGGCCTCTG CTTGTCCTCCCTGGCCTCCTGAGAG CCTCAGGCTCTGGCCCAACATATT CCAATACCTTGGCCAAAACAGAGG TCCAGGGGGCCTCCTGCCACCTTG AGTATAGTCCAGAACGAGGCAAAG CTGAAGGCAGA<3' (SEQ ID NO: 4)
---	---

FIG. 2B

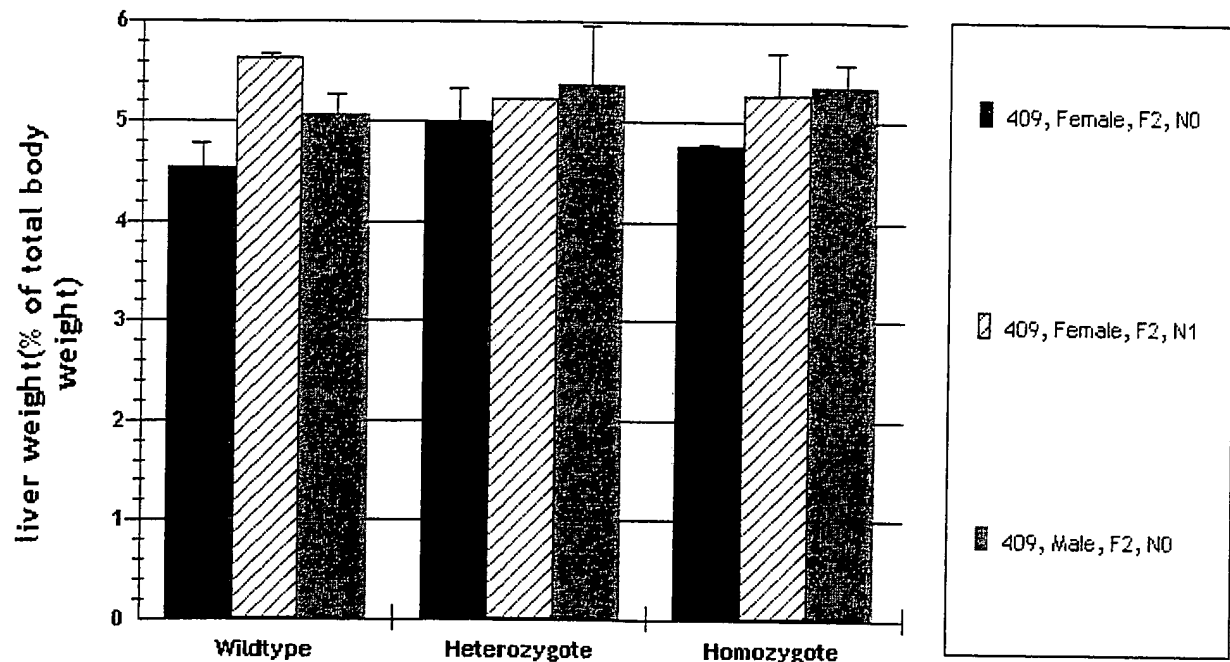
## necropsy - spleen weight/body weight



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FIG. 3

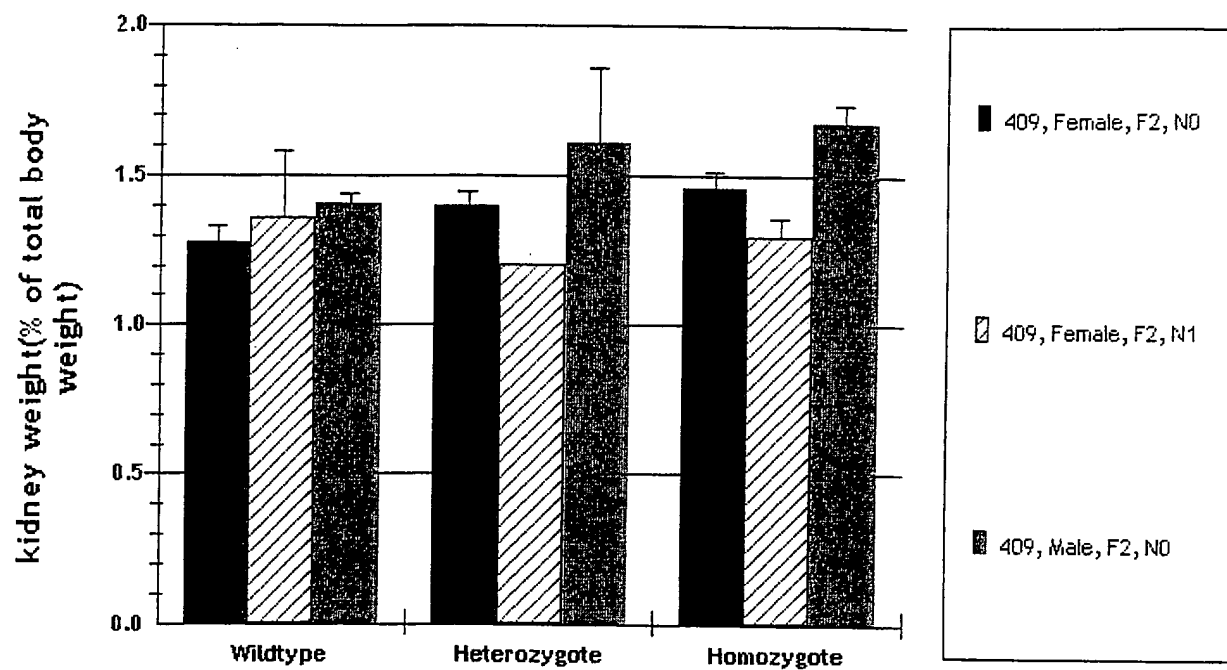
## necropsy - liver weight/body weight



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FIG. 4

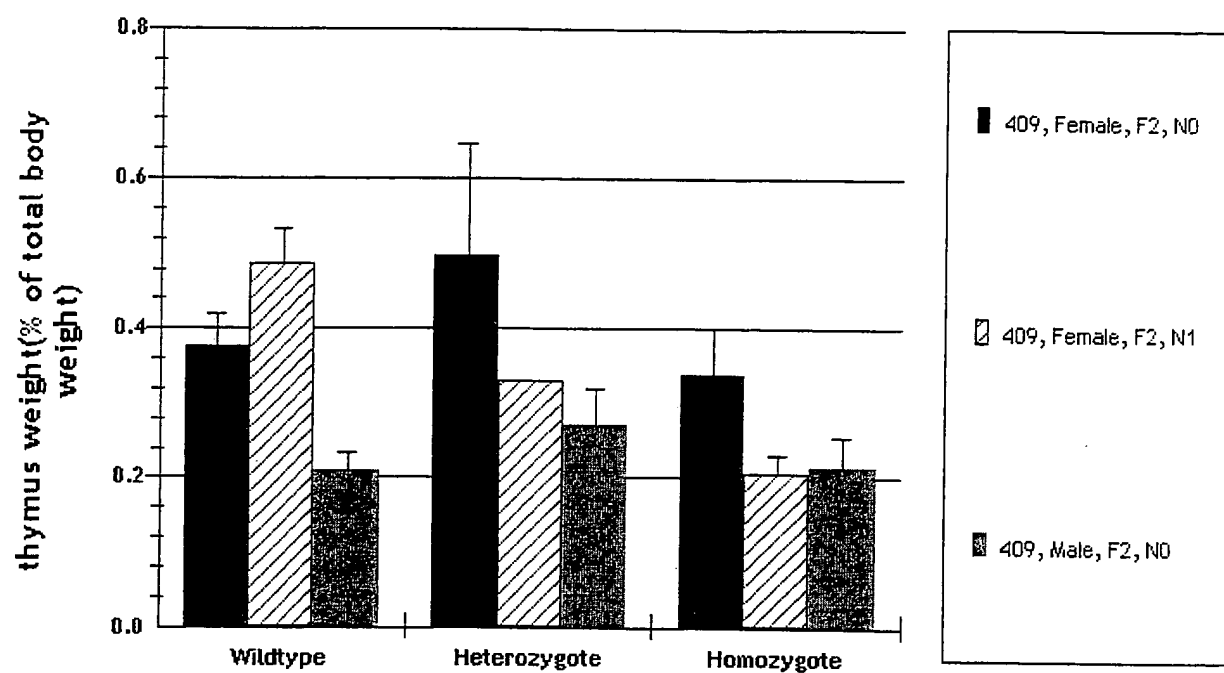
## necropsy - kidney weight/body weight



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FIG. 5

## necropsy - thymus weight/body weight



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FIG. 6